

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/041,054A
Source: IFW16
Date Processed by STIC: 1/3/05

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IFW16

RAW SEQUENCE LISTING

DATE: 01/03/2005

PATENT APPLICATION: US/10/041,054A

TIME: 16:53:27

Input Set : A:\ORT1560NP.Subst.Seq.List.txt

Output Set: N:\CRF4\01032005\J041054A.raw

3 <110> APPLICANT: Darrow, Andrew
 4 Qi, Jenson
 5 Andrade-Gordon, Patricia
 7 <120> TITLE OF INVENTION: DNA ENCODING THE HUMAN SERINE PROTEASE T
 9 <130> FILE REFERENCE: ORT-1560
 11 <140> CURRENT APPLICATION NUMBER: 10/041,054A
 12 <141> CURRENT FILING DATE: 2002-01-07
 14 <150> PRIOR APPLICATION NUMBER: 09/386,653
 15 <151> PRIOR FILING DATE: 1999-08-31
 17 <160> NUMBER OF SEQ ID NOS: 11
 19 <170> SOFTWARE: PatentIn version 3.3
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1110
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Homo sapiens
 26 <400> SEQUENCE: 1

27	gaccacggcc	ctgcggccca	gccaggcctg	aggacatgag	gccccggcg	gcgggtgcgc	60
29	tcctgctgt	gctgtttt	gggtctcaga	ggccaaggc	agcaacagcc	tgtggtcgc	120
31	ccaggatgt	gaaccgaatg	gtggggcggc	aggacacgc	ggagggcgag	tggccctggc	180
33	aagtcatgt	ccagcgcaac	ggaagccact	tctgcgggg	cagcctcatc	gcggagcagt	240
35	gggtcctgac	ggctgcgcac	tgcttccgca	acacccctga	gacgtccctg	taccaggtcc	300
37	tgtctggggc	aaggcagcta	gtgcagccgg	gaccacacgc	tatgtatgcc	cgggtgaggc	360
39	agtgaggag	caaccctctg	taccaggcga	cggcctccag	cgctgacgtg	gccctggtgg	420
41	agctggaggc	accagtgcac	ttcaccaatt	acatcctccc	cgtgtccctg	cctgaccct	480
43	cggtgatctt	tgagacgggc	atgaactgt	gggtcactgg	ctggggcagc	cccaagtgg	540
45	aagacccct	gcccgaaccg	cgatcctgc	agaaactcgc	tgtgcccac	atcgacacac	600
47	ccaaatgtcaa	cctgctctac	agcaaagaca	ccgagtttgg	ctaccaaccc	aaaaccatca	660
49	agaatgacat	gctgtgcgac	ggcttcgagg	agggcaagaa	ggatgcctgc	aaggcgact	720
51	cggggggccc	cctgggtgc	ctcgtgggtc	agtcgtggct	gcaggcgggg	gtgatcagct	780
53	gggggtgaggg	ctgtccccgc	cagaaccggc	cagggtctta	catccgtgtc	accgcccacc	840
55	acaactggat	ccatcgatc	atccccaaac	tgcagttcca	gccagcgagg	ttggggcggcc	900
57	agaagtggaa	ccccccccggc	caggagcccc	ttgagcagag	ctctgcaccc	agctgcccgg	960
59	cccacaccat	cctgctggtc	ctccccagcgc	tgctgttgca	cctgtgagcc	ccaccagact	1020
61	catttgtaaa	tagcgtctt	tcctcccttc	tcaaataccc	ttattttatt	tatgtttctc	1080
63	ccaaataaaaa	cccgccctgt	gtgccagctg				1110
66	<210>	SEQ ID NO:	2				
67	<211>	LENGTH:	20				
68	<212>	TYPE:	DNA				
69	<213>	ORGANISM:	Artificial				
71	<220>	FEATURE:					
72	<223>	OTHER INFORMATION:	ProtT PCRTP-U PCR primer				
74	<400>	SEQUENCE:	2				
75	gcccaggcctg	aggacatgag					20

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78 <210> SEQ ID NO: 3
79 <211> LENGTH: 20
80 <212> TYPE: DNA
81 <213> ORGANISM: Artificial
83 <220> FEATURE:
84 <223> OTHER INFORMATION: ProtT PCRTP-L PCR primer
86 <400> SEQUENCE: 3
87 tgccgtggat gctgacttgc 20
90 <210> SEQ ID NO: 4
91 <211> LENGTH: 40
92 <212> TYPE: DNA
93 <213> ORGANISM: Artificial
95 <220> FEATURE:
96 <223> OTHER INFORMATION: ProtT PCTTP-PP primer
98 <400> SEQUENCE: 4
99 ccaggatgct gaaccgaatg gtgggcgggc aggacacgca 40
102 <210> SEQ ID NO: 5
103 <211> LENGTH: 30
104 <212> TYPE: DNA
105 <213> ORGANISM: Artificial
107 <220> FEATURE:
108 <223> OTHER INFORMATION: ProtT Xba-U PCR primer
110 <400> SEQUENCE: 5
111 aggatctaga ggagggcgag tggccctggc 30
114 <210> SEQ ID NO: 6
115 <211> LENGTH: 30
116 <212> TYPE: DNA
117 <213> ORGANISM: Artificial
119 <220> FEATURE:
120 <223> OTHER INFORMATION: ProtT Xba-L PCR primer
122 <400> SEQUENCE: 6
123 ggggtctaga cttctggccg cccaacctcg 30
126 <210> SEQ ID NO: 7
127 <211> LENGTH: 290
128 <212> TYPE: PRT
129 <213> ORGANISM: Homo sapiens
131 <400> SEQUENCE: 7
133 Met Arg Arg Pro Ala Ala Val Pro Leu Leu Leu Leu Cys Phe Gly
134 1 5 10 15
137 Ser Gln Arg Ala Lys Ala Ala Thr Ala Cys Gly Arg Pro Arg Met Leu
138 20 25 30
141 Asn Arg Met Val Gly Gly Gln Asp Thr Gln Glu Gly Glu Trp Pro Trp
142 35 40 45
145 Gln Val Ser Ile Gln Arg Asn Gly Ser His Phe Cys Gly Gly Ser Leu
146 50 55 60
149 Ile Ala Glu Gln Trp Val Leu Thr Ala Ala His Cys Phe Arg Asn Thr
150 65 70 75 80
153 Ser Glu Thr Ser Leu Tyr Gln Val Leu Leu Gly Ala Arg Gln Leu Val
154 85 90 95

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157 Gln Pro Gly Pro His Ala Met Tyr Ala Arg Val Arg Gln Val Glu Ser
158 100 105 110
161 Asn Pro Leu Tyr Gln Gly Thr Ala Ser Ser Ala Asp Val Ala Leu Val
162 115 120 125
165 Glu Leu Glu Ala Pro Val Pro Phe Thr Asn Tyr Ile Leu Pro Val Cys
166 130 135 140
169 Leu Pro Asp Pro Ser Val Ile Phe Glu Thr Gly Met Asn Cys Trp Val
170 145 150 155 160
173 Thr Gly Trp Gly Ser Pro Ser Glu Glu Asp Leu Leu Pro Glu Pro Arg
174 165 170 175
177 Ile Leu Gln Lys Leu Ala Val Pro Ile Ile Asp Thr Pro Lys Cys Asn
178 180 185 190
181 Leu Leu Tyr Ser Lys Asp Thr Glu Phe Gly Tyr Gln Pro Lys Thr Ile
182 195 200 205
185 Lys Asn Asp Met Leu Cys Ala Gly Phe Glu Glu Gly Lys Lys Asp Ala
186 210 215 220
189 Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Leu Val Gly Gln Ser
190 225 230 235 240
193 Trp Leu Gln Ala Gly Val Ile Ser Trp Gly Glu Gly Cys Ala Arg Gln
194 245 250 255
197 Asn Arg Pro Gly Val Tyr Ile Arg Val Thr Ala His His Asn Trp Ile
198 260 265 270
201 His Arg Ile Ile Pro Lys Leu Gln Phe Gln Pro Ala Arg Leu Gly Gly
202 275 280 285
205 Gln Lys
206 290
209 <210> SEQ ID NO: 8
210 <211> LENGTH: 1130
211 <212> TYPE: DNA
212 <213> ORGANISM: Artificial
214 <220> FEATURE:
215 <223> OTHER INFORMATION: PFEK-PROTT-HIS fusion protein nucleic acid sequence
217 <400> SEQUENCE: 8
218 gaattcacca ccatggacag caaagggtcg tcgcagaaat cccgcctgct cctgctgctg 60
220 gtgggtgtcaa atctactctt gtgccaggg gtggtctccg actacaagga cgacgcacgac 120
222 gtggacgcgg cccgtcttgc tgcccccttt gatgatgatg acaagatcgt tgggggctat 180
224 gctctagagg agggcgagtg gcccggcaa gtcagcatcc agcgcaacgg aagccacttc 240
226 tgccccggca gcctcatcgc ggagcagttg gtcctgacgg ctgcgcactg cttccgcaac 300
228 acctctgaga cgtccctgtt ccaggtcctg ctgggggcaa ggcagctagt gcagccggaa 360
230 ccacacgcta tgtatgcccc ggtgaggccag gtggagagca acccccgtt ccagggcacc 420
232 gctccagcg ctgacgtggc cctggtgag ctggaggcac cagtgcctt caccattac 480
234 atcctccccc tgtgcctgcc tgacccctcg gtatcttg agacggcat gaactgctgg 540
236 gtcactggct gggcagccc cagtgagaa gacccctcgc cccaaaccgcg gatcctgcag 600
238 aaactcgctg tgcccatcat cgacacaccc aagtgcaccc tgctctacag caaagacacc 660
240 gagtttgctt accaacccaa aaccatcaag aatgacatgc tgtgcggcg cttcgaggag 720
242 ggcaagaagg atgcctgcaa gggcgactcg ggccggccccc tgggtgcct cgtgggtcag 780
244 tcgtggctcg aggccccgg gatcagctgg ggtgagggt gtgcccggca gaaccggccca 840
246 ggtgtctaca tccgtgtcac cggccaccac aactggatcc atcggatcat ccccaaactg 900
248 cagttccagc cagcgaggtt gggcgccag aagtctagac atcaccatca ccatcactag 960

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250 cggccgcttc ccttagtga gggtaatgc ttgcagcaga catgataaga tacattgtg 1020
 252 agttggaca aaccacaact agaatgcagt gaaaaaaatg ctattttgt gaaatttg 1080
 254 atgctattgc ttatgtta accattataa gctgcaataa acaagttgac 1130
 257 <210> SEQ ID NO: 9
 258 <211> LENGTH: 315
 259 <212> TYPE: PRT
 260 <213> ORGANISM: Artificial
 262 <220> FEATURE:
 263 <223> OTHER INFORMATION: PFEK-PROTT-HIS fusion protein amino acid sequence
 265 <400> SEQUENCE: 9
 267 Met Asp Ser Lys Gly Ser Ser Gln Lys Ser Arg Leu Leu Leu Leu 1
 268 1 5 10 15
 271 Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr Lys
 272 20 25 30
 275 Asp Asp Asp Asp Val Asp Ala Ala Ala Leu Ala Ala Pro Phe Asp Asp
 276 35 40 45
 279 Asp Asp Lys Ile Val Gly Gly Tyr Ala Leu Glu Glu Gly Glu Trp Pro
 280 50 55 60
 283 Trp Gln Val Ser Ile Gln Arg Asn Gly Ser His Phe Cys Gly Gly Ser
 284 65 70 75 80
 287 Leu Ile Ala Glu Gln Trp Val Leu Thr Ala Ala His Cys Phe Arg Asn
 288 85 90 95
 291 Thr Ser Glu Thr Ser Leu Tyr Gln Val Leu Leu Gly Ala Arg Gln Leu
 292 100 105 110
 295 Val Gln Pro Gly Pro His Ala Met Tyr Ala Arg Val Arg Gln Val Glu
 296 115 120 125
 299 Ser Asn Pro Leu Tyr Gln Gly Thr Ala Ser Ser Ala Asp Val Ala Leu
 300 130 135 140
 303 Val Glu Leu Glu Ala Pro Val Pro Phe Thr Asn Tyr Ile Leu Pro Val
 304 145 150 155 160
 307 Cys Leu Pro Asp Pro Ser Val Ile Phe Glu Thr Gly Met Asn Cys Trp
 308 165 170 175
 311 Val Thr Gly Trp Gly Ser Pro Ser Glu Glu Asp Leu Leu Pro Glu Pro
 312 180 185 190
 315 Arg Ile Leu Gln Lys Leu Ala Val Pro Ile Ile Asp Thr Pro Lys Cys
 316 195 200 205
 319 Asn Leu Leu Tyr Ser Lys Asp Thr Glu Phe Gly Tyr Gln Pro Lys Thr
 320 210 215 220
 323 Ile Lys Asn Asp Met Leu Cys Ala Gly Phe Glu Glu Gly Lys Lys Asp
 324 225 230 235 240
 327 Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Leu Val Gly Gln
 328 245 250 255
 331 Ser Trp Leu Gln Ala Gly Val Ile Ser Trp Gly Glu Gly Cys Ala Arg
 332 260 265 270
 335 Gln Asn Arg Pro Gly Val Tyr Ile Arg Val Thr Ala His His Asn Trp
 336 275 280 285
 339 Ile His Arg Ile Ile Pro Lys Leu Gln Phe Gln Pro Ala Arg Leu Gly
 340 290 295 300
 343 Gly Gln Lys Ser Arg His His His His His His

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Input Set : A:\ORT1560NP.Subst.Seq.List.txt

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344 305 310 315
347 <210> SEQ ID NO: 10
348 <211> LENGTH: 4
349 <212> TYPE: PRT
350 <213> ORGANISM: Artificial
352 <220> FEATURE:
353 <223> OTHER INFORMATION: Chromogenic substrate 5
356 <220> FEATURE:
357 <221> NAME/KEY: MISC_FEATURE
358 <222> LOCATION: (1)..(1)
359 <223> OTHER INFORMATION: N-Succinyl-alanine
361 <220> FEATURE:
362 <221> NAME/KEY: MISC_FEATURE
363 <222> LOCATION: (4)..(4)
364 <223> OTHER INFORMATION: Phe-p-nitroanilide
366 <400> SEQUENCE: 10
W--> 368 Xaa Ala Pro Xaa
369 1
372 <210> SEQ ID NO: 11
373 <211> LENGTH: 4
374 <212> TYPE: PRT
375 <213> ORGANISM: Artificial
377 <220> FEATURE:
378 <223> OTHER INFORMATION: Chromogenic substrate 6
381 <220> FEATURE:
382 <221> NAME/KEY: MISC_FEATURE
383 <222> LOCATION: (1)..(1)
384 <223> OTHER INFORMATION: N- (methoxysuccinyl) -Ala
386 <220> FEATURE:
387 <221> NAME/KEY: MISC_FEATURE
388 <222> LOCATION: (4)..(4)
389 <223> OTHER INFORMATION: Val-p-nitroanilide
391 <400> SEQUENCE: 11
W--> 393 Xaa Ala Pro Xaa
394 1

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:10; Xaa Pos. 1,4
Seq#:11; Xaa Pos. 1,4

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:2,3,4,5,6,8,9,10,11

VERIFICATION SUMMARY

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Input Set : A:\ORT1560NP.Subst.Seq.List.txt

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L:368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:393 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0